

IN THE CLAIMS

This listing of claims replaces all prior versions, and listings, in this application.

1. (original) An isolated HXT3 hexose transporter or functional fragments thereof with an improved capacity to transport carbohydrates.

2. (previously presented) An isolated HXT3 hexose transporter having an improved capacity to transport fructose with respect to the capacity to transport fructose of a wild type hexose transporter having SEQ ID NO: 26.

3. (previously presented) The HXT3 hexose transporter according to claim 1, having an amino acid sequence selected from the group consisting of:

- a sequence derived from SEQ ID NO: 26 and having at least a mutation at a position selected from the group consisting of Gln 206, Leu 207, Met 208, Ile 209, Thr 210, Leu 211 and Gly 212; or
- SEQ ID NO: 27.

4. (previously presented) The HXT3 hexose transporter according to claim 3, additionally comprising at least a mutation at a position selected from the group consisting of Met 324, Leu 388, Ile 392, Glu 414, Gly 415, Ile 449 and Leu 471.

5. (currently amended) An isolated nucleic acid encoding a mutated [[the]] HXT3 hexose transporter, which comprises a nucleotide sequence encoding an amino acid sequence with one or more mutations in comparison with SEQ ID NO: 26 according to claim 1.

6. (previously presented) The nucleic acid according to claim 5, having a sequence according to SEQ ID NO: 28, SEQ ID NO: 29 or a functional homologue thereof.

7. (previously presented) Recombinant yeast cell transformed with a nucleic acid according to claim 5.

8. (original) Process for obtaining a yeast cell with improved fructophilic properties wherein a yeast cell comprising a gene encoding an HXT3 transporter has been altered in such a way that the HXT3 transporter has an improved capacity to transport fructose, comprising the steps of:

- a. mutating the HXT3 gene and
- b. selecting the yeast cell with improved fructophilic properties.

9. (original) Yeast cell obtainable by the process according to claim 8.

10. (previously presented) Yeast cell according to claim 7, wherein the yeast is *Saccharomyces cerevisiae*, *S. uvarum*, *S. bayanus*, *S. pastorianus* or *S. paradoxus*.

11. (currently amended) A method [[Use]] of using a yeast cell according to claim 7, the method comprising: fermenting 9 for fermentation of carbohydrates with the yeast cell.

12. (previously presented) The HXT3 hexose transporter according to claim 1, having an amino acid sequence which is a sequence derived from SEQ ID NO: 26 and having at least a mutation at a position at Ile 209.

13. (previously presented) The HXT3 hexose transporter according to claim 3, additionally comprising at least a mutation selected from the group consisting of Met 324 Ile, Leu 388 Met, Tyr 389 Trp, Ile 392 Val, Glu 414 Gln, Gly 415 Asn, Ile 449 Val and Leu 471 Ile.

14. (new) An isolated nucleic acid encoding a mutated HXT3 hexose transporter with an improved capacity to transport carbohydrates as compared to a wild-type hexose transporter encoded by SEQ ID NO: 26.

15. (new) The nucleic acid according to claim 14, which comprises the nucleotide sequence of SEQ ID NO: 28.

16. (new) The nucleic acid according to claim 14, which encodes an amino acid sequence selected from the group consisting of:

- a sequence derived from SEQ ID NO: 26 and having at least a mutation at a position selected from the group consisting of Gln 206, Leu 207, Met 208, Ile 209, Thr 210, Leu 211 and Gly 212; or
- SEQ ID NO: 27.

17. (new) The nucleic acid according to claim 14, which encodes an amino acid sequence derived from SEQ ID NO: 26 and having at least a mutation at a position selected from the group consisting of Gln 206, Leu 207, Met 208, Ile 209, Thr 210, Leu 211 and Gly 212, and further comprising at least a mutation at a position selected from the group consisting of Met 324, Leu 388, Ile 392, Glu 414, Gly 415, Ile 449 and Leu 471.

18. (new) The nucleic acid according to claim 14, which encodes an amino acid sequence derived from SEQ ID NO: 26 and having at least a mutation at a position at Ile 209.

19. (new) The nucleic acid according to claim 14, which encodes an amino acid sequence derived from SEQ ID NO: 26 and having at least a mutation at a position selected from the group consisting of Gln 206, Leu 207, Met 208, Ile 209, Thr 210, Leu 211 and Gly 212, and further comprising at least a mutation selected from the group consisting of Met 324, Leu 388, Tyr 389, Ile 392, Glu 414, Gly 415, Ile 449 and Leu 471 Ile.